

Scientists develop method to find genetic basis for plant variation

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A new research approach that allowed scientists to rapidly identify the gene responsible for high sodium levels in certain naturally occurring plant populations could have applications for the study of a wide variety of other important plant properties.

The approach, a combination of new and existing technologies, may offer researchers a tool to pinpoint genetic differences many times faster than currently possible and help shed light on the likely origin of such differences.

"We've combined a variety of techniques to get at the gene behind a specific trait," said David Salt, a horticulture professor at Purdue University. "If picked up broadly, the approach could have an important impact on the activities of other laboratories."

The method allowed Salt's research team to determine differences within a single gene that drives a specific trait among naturally occurring plant populations -- a finding that can take years with current methods, he said.

Salt's method combines the new technology of DNA microarrays with information from a large genetic database in order to sidestep the lengthy processes previously used to identify similar genetic variations. Salt employed his methodology to identify a sodium-regulating gene in the extensively studied *Arabidopsis thaliana*, a wild mustard plant.

Salt said this approach could allow scientists to better understand the genetic basis of naturally occurring variations. These variations occur in the manifestation of tangible traits, or phenotypes, within a single species. Phenotypic differences can include anything from flower color to cold sensitivity or sodium concentration. This ubiquitous tendency of individuals and populations to vary is termed natural variation.

Evolutionary theory proposes that differences among populations can arise for evolutionarily favorable, or adaptive, reasons. If the differences between populations become great enough, they might lead to the development of a new species, called speciation.

The mechanism of speciation, however, remains poorly understood. Salt said this approach could hopefully shed light on the process.

"By looking at natural variation, which we assume to be adaptive, we might be able to better understand why the organism evolved to be that way," Salt said. "This could be of value in many areas of biology."

Salt's findings were published earlier this month in the online journal PLoS Genetics.

Salt studies the composition of elements and ions, tiny charged particles, in plants. Called ionomics, the study of a plant's elemental composition is important for understanding their physiology, Salt said.

Since plants are immobile, they must make the most of their environment -- the water, sunlight and soil where they are -- to survive. Plants' ability to survive and thrive is tied to their ability to take up the right chemicals, usually in ionic form, from the soil.

Salt uses the database, known as the Purdue Ionomics Information Management System (PiiMS), to find "candidate genes," or genes that warrant further study. He combines this knowledge with results from

DNA microarrays, small chips that can identify miniscule genetic differences between populations of a single species.

In the Arabidopsis study, Salt identified the gene, called AtHKT1, responsible for elevated sodium levels in two wild populations of the plant. The study began with a simple observation: Two populations of Arabidopsis from coastal regions of Spain and Japan had inexplicably high levels of sodium.

"So, the question became, 'Why?' But to get there, we had to first answer a series of simpler questions," Salt said.

The first question was how those plants differ from the "garden-variety" Arabidopsis. This is not a simple question, he said, which is why so few studies have been published concerning the precise genetic basis of natural variation.

The initial difficulty is that to date only one variety of Arabidopsis has had its genetic material sequenced. But this particular variety, called Col-0 (so named because it is indigenous to Colombia), is not genetically identical to all other populations of Arabidopsis, Salt said.

For an answer, Salt used DNA microarrays to detect genes that varied in the two coastal populations. He cross-referenced this information with the database to seek out genetic differences that may play a role in regulating sodium levels.

Salt found that the coastal populations had a different version of the gene called AtHKT1, which previous studies have shown helps govern the process in which sodium is prevented from rising out of the plant's roots.

Further experiments showed that AtHKT1 is genetically associated with sodium tolerance, which could help explain why the gene is found in

coastal populations where there may be elevated salt levels.

"It could just be a coincidence that these coastal populations, where soils naturally have higher sodium concentrations, have a defective version of a gene involved in sodium regulation," Salt said, "But it also may not be. We are currently in the process of answering the original question of why. This methodology has gotten us very close to an explanation."

Sodium chloride, or table salt, is generally toxic to plants at significantly high concentrations. Salt said this study will help his team better understand the way in which plants process sodium.

Postdoctoral researchers Ana Rus and Ivan Baxter co-authored the paper. Salt is currently investigating the potential origin of the defective AtHKT1 gene.

He continues to add to his database, compiling thousands of samples a week. His database records what Arabidopsis genes have been "knocked out," or mutated, and lists the corresponding levels of 17 different elements in each plant. A paper describing this PiiMS database has been accepted for publication in the journal Plant Physiology.

The database can be accessed online at <http://www.purdue.edu/dp/ionomics>.

Source: Purdue University

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